

Serial No.: 09/954,737  
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**Amendments to the Specification**

The following is a marked-up version the Specification pursuant to revised 37 C.F.R. §1.121, with instructions and markings showing changes made herein to the Specification as filed. Underlining denotes added text while brackets denote deleted text.

On page 7, please replace the paragraph starting on line 14 with the following:

**Fig 7. Predicted twin-arginine (RR-)signal peptides of *B. subtilis*.** The listed signal peptides (SEQ ID NOS:30-51) contain, in addition to the twin-arginines, at least one other residue of the consensus sequence (R-R-X-ΦΦ; printed in bold). The number of residues in the N- and H-domains of each signal peptide, and the average hydrophobicity (h) of each of these domains, as determined by the algorithms of Kyte and Doolittle (Kyte, J., and R. F. Doolittle [1982] A simple method for displaying the hydropathic character of a protein. J. Mol. Biol. 157:105-32), are indicated. Furthermore, the RR-motifs in the N-domain, and SPase I recognition sites in the C-domain (ie. positions -3 to -1 relative to the predicted SPase cleavage site) are shown. Proteins lacking a (putative) SPase I cleavage site, some of which contain additional transmembrane domains, are indicated with "TM". One protein containing cell wall binding repeats is indicated with "W".

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